

SEQUENCE LISTING

<110> Presnell, Scott R.
 Xu, Wenfeng
 Novak, Julia E.
 Whitmore, Theodore E.
 Grant, Francis J.

<120> CYTOKINE RECEPTOR ZCYTOR19

<130> 00-108

<150> US 60/253,561

<151> 2000-11-28

<150> US 60/267,211

<151> 2001-02-07

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<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1476

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1473)

<400> 1

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gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg	96
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu	
20 25 30	
ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc	144

0995898-11301

Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly	
35 40 45	
aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc	192
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr	
50 55 60	
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg	240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu	
65 70 75 80	
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc	288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe	
85 90 95	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg	336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	
100 105 110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct	384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro	
115 120 125	
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg	432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr	
130 135 140	
tac cag ctg ccc ccc tgc atg ccc cca ctg ttt ctg aag tat gag gtg	480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val	
145 150 155 160	
gca ttt tgg ggg ggg ggg gcc gga acc aag acc cta ttt cca gtc act	528
Ala Phe Trp Gly Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr	
165 170 175	
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa	576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu	
180 185 190	
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa	624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys	
195 200 205	

0095898-12801

tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa	672
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu	
210 215 220	
gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta	720
Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu	
225 230 235 240	
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc	768
Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro	
245 250 255	
tgg ttt cag cgg gca aag atg cca cgg gcc ctg gaa ctg acc aga ggg	816
Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Glu Leu Thr Arg Gly	
260 265 270	
gtc agg ccg acg cct cga gtc agg gcc cca gcc acc caa cag aca aga	864
Val Arg Pro Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg	
275 280 285	
tgg aag aag gac ctt gca gag gac gaa gag gag gag gat gag gag gac	912
Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp	
290 295 300	
aca gaa gat ggc gtc agc ttc cag ccc tac att gaa cca cct tct ttc	960
Thr Glu Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe	
305 310 315 320	
ctg ggg caa gag cac cag gct cca ggg cac tcg gag gct ggt ggg gtg	1008
Leu Gly Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val	
325 330 335	
gac tca ggg agg ccc agg gct cct ctg gtc cca agc gaa ggc tcc tct	1056
Asp Ser Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser	
340 345 350	
gct tgg gat tct tca gac aga agc tgg gcc agc act gtg gac tcc tcc	1104
Ala Trp Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser	
355 360 365	
tgg gac agg gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc	1152
Trp Asp Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly	
370 375 380	

00055898 "12801

caa ggg ccg ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa 1200
 Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
 385 390 395 400

ttc tcc aag gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc 1248
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
 405 410 415

tcc tcc tgg gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc 1296
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
 420 425 430

cct ggg gga ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa 1344
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
 435 440 445

agc agc cct gag gag gaa gag gag gcg agg gaa tca gaa att gag gac 1392
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
 450 455 460

agc gat gcg ggc agc tgg ggg gct gag agc acc cag agg acc gag gac 1440
 Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
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agg ggc cgg aca ttg ggg cat tac atg gcc agg tga 1476
 Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg
 485 490

<210> 2

<211> 491

<212> PRT

<213> Homo sapiens

<400> 2

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 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45

Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr
50						55					60				
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
65					70					75					80
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
				85					90					95	
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
			100					105					110		
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
		115					120					125			
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
						135						140			
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Phe	Leu	Lys	Tyr	Glu	Val
145					150					155					160
Ala	Phe	Trp	Gly	Gly	Gly	Ala	Gly	Thr	Lys	Thr	Leu	Phe	Pro	Val	Thr
				165					170					175	
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu
			180					185					190		
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys
		195					200					205			
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu
		210				215					220				
Ala	Asn	Trp	Ala	Phe	Leu	Val	Leu	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu
225					230					235					240
Val	Ile	Ala	Ala	Gly	Gly	Val	Ile	Trp	Lys	Thr	Leu	Met	Gly	Asn	Pro
				245					250					255	
Trp	Phe	Gln	Arg	Ala	Lys	Met	Pro	Arg	Ala	Leu	Glu	Leu	Thr	Arg	Gly
			260					265					270		
Val	Arg	Pro	Thr	Pro	Arg	Val	Arg	Ala	Pro	Ala	Thr	Gln	Gln	Thr	Arg
		275					280					285			
Trp	Lys	Lys	Asp	Leu	Ala	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Asp
		290				295				300					
Thr	Glu	Asp	Gly	Val	Ser	Phe	Gln	Pro	Tyr	Ile	Glu	Pro	Pro	Ser	Phe
305					310					315					320
Leu	Gly	Gln	Glu	His	Gln	Ala	Pro	Gly	His	Ser	Glu	Ala	Gly	Gly	Val
				325					330					335	
Asp	Ser	Gly	Arg	Pro	Arg	Ala	Pro	Leu	Val	Pro	Ser	Glu	Gly	Ser	Ser
			340					345				350			
Ala	Trp	Asp	Ser	Ser	Asp	Arg	Ser	Trp	Ala	Ser	Thr	Val	Asp	Ser	Ser
		355					360					365			
Trp	Asp	Arg	Ala	Gly	Ser	Ser	Gly	Tyr	Leu	Ala	Glu	Lys	Gly	Pro	Gly
		370					375				380				

0995898-112801

Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
 385 390 395 400
 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
 405 410 415
 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
 420 425 430
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
 435 440 445
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
 450 455 460
 Ser Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp
 465 470 475 480
 Arg Gly Arg Thr Leu Gly His Tyr Met Ala Arg
 485 490

<210> 3

<211> 1473

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide seuquence of SEQ ID NO:2

<221> misc_feature

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<223> n = A,T,C or G

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ytnacntggy tncnggnyy nggnaayccn caryaygt na cntayttygt ngcntaycar	180
wsnwsnccna cmgmngnm ntggmgngar gtngargart gygcnggnac naargarytn	240
ytntgywsna tgatgtgyyt naaraarcar gayytnaya ayaarttyaa rggmngngtn	300
mgnacngtnw snccnwsnws naarwsnccn tgggtngarw sngartayyt ngaytayytn	360
ttygargtng arcngcncnc nccngtnytn gtnytnacnc araccngarga rathytnwsn	420
gcnaaygcna cntaycaryt nccncntgy atgcncncny tnttyytnaa rtaygargtn	480
gcnttytggg gnggngngc nggnacnaar acnytnnttyc cngtnacncc ncayggncar	540
ccngtnccara thacnytnca rccngcngcn wsnargcayc aytgyytnws ngcncmgnacn	600
athtayacnt tywsngtncc naartaywsn aarttywsna arccnacntg yttyytnytn	660
gargtnccng argcnaaytg ggcnttyytn gtnytnccnw snytnytnat hytnytnytn	720
gtnathgcng cnggngnggt nathtggaar acnytnatgg gnaayccntg gttycarmgn	780
gcnaaratgc cmgmngcny ngarytnacn mgngnggtm gncnacncc nmngngtnmgn	840
gcncngcna cncarcarac nmngtggaar aargayytn cngargayga rgargargar	900

gaygargarg ayacngarga yggngtnwsn titycarcnt ayathgarcc nccnwsntty 960
 ytnggncarg arcaycargc nccnggncay wsnrgargcng gngngtnga ywsnggmgn 1020
 ccmngngcnc cnytngtncc nwsngarggn wsnwsngcnt gggaywsnws ngaymgnwsn 1080
 tgggcnwsna cngtngayws nwsntgggay mgngcnggnw snwsnggnta yytngcngar 1140
 aarggncng gncarggnc ngnggngay ggncaycarg arwsnytncc nccnccngar 1200
 ttywsnaarg aywsnggntt yytngargar ytncngarg ayaaytnws nwsntgggcn 1260
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 caracnytna cnttytytg ggarwsnwsn ccngargarg argargargc nmngarwsn 1380
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<211> 203

<212> PRT

<213> Homo sapiens

<400> 4

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 Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr Arg Arg Arg Trp
 35 40 45
 Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu Leu Cys Ser Met
 50 55 60
 Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe Lys Gly Arg Val
 65 70 75 80
 Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val Glu Ser Glu Tyr
 85 90 95
 Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro Val Leu Val Leu
 100 105 110
 Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr Tyr Gln Leu Pro
 115 120 125
 Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val Ala Phe Trp Gly
 130 135 140
 Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr Pro His Gly Gln
 145 150 155 160
 Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu His His Cys Leu
 165 170 175
 Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys Tyr Ser Lys Phe
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 Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro
 195 200

TOGETHER "112001" 88888888

<210> 5
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 <213> Artificial Sequence

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 <223> WSXWS motif

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 <223> Xaa = Any Amino Acid

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<210> 6
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<220>
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<400> 6
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 <211> 23
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<210> 8
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<223> Oligonucleotide primer ZC14063

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<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC17574

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<212> PRT

<213> Artificial Sequence

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<223> Glu-Glu peptide tag

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Glu Tyr Met Pro Met Glu

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<210> 12

<211> 8

0995598-112801

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20 25 30	
ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc	144
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser	
35 40 45	
ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc	192
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser	
50 55 60	
ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc	240
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr	
65 70 75 80	
tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag	288
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys	
85 90 95	
aaa gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc	336
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys	
100 105 110	
cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca	384
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro	
115 120 125	
aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc	432
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys	
130 135 140	
gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg	480
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp	
145 150 155 160	
tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag	528
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu	
165 170 175	
gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg	576
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu	
180 185 190	

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cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac	624
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn	
195 200 205	
aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg	672
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly	
210 215 220	
cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag	720
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu	
225 230 235 240	
ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat	768
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr	
245 250 255	
ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac	816
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn	
260 265 270	
aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc	864
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe	
275 280 285	
ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac	912
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn	
290 295 300	
gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg	960
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr	
305 310 315 320	
cag aag agc ctc tcc ctg tct ccg ggt aaa	990
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
325 330	

<210> 15

<211> 330

<212> PRT

<213> Homo sapiens

0995898.12301

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 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

09995898 "112301

<210> 16
 <211> 321
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(321)

<400> 16
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 ttg aaa tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat 96
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 20 25 30
 ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg 144
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 35 40 45
 ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc 192
 Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 50 55 60
 tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa 240
 Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 65 70 75 80
 cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc 288
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 85 90 95
 gtc aca aag agc ttc aac agg gga gag tgt tag 321
 Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
 100 105

<210> 17
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 <212> PRT

0995593.1.2001

<213> Homo sapiens

<400> 17

Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln
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Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr
			20					25					30		
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser
			35				40					45			
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr
	50					55				60					
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys
65					70					75				80	
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro
				85				90						95	
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys						
			100					105							

<210> 18

<211> 1563

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1563)

<400> 18

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Met	Ala	Gly	Pro	Glu	Arg	Trp	Gly	Pro	Leu	Leu	Leu	Cys	Leu	Leu	Gln	
1				5				10						15		
gcc	gct	cca	ggg	agg	ccc	cgt	ctg	gcc	cct	ccc	cag	aat	gtg	acg	ctg	96
Ala	Ala	Pro	Gly	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu	
			20					25					30			
ctc	tcc	cag	aac	ttc	agc	gtg	tac	ctg	aca	tgg	ctc	cca	ggg	ctt	ggc	144
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly	
			35				40					45				
aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	192
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
			50				55				60					

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cg	t	aga	cg	g	tg	gc	gaa	gt	gaa	ga	gt	gc	gga	acc	aag	ga	ct	g	240
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu				
65					70					75							80		
cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc				288
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe				
				85					90						95				
aag	gga	cg	gt	cg	ac	gt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg				336
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val				
			100					105						110					
gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct				384
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro				
		115					120						125						
gtc	ctg	gtg	ctc	acc	cag	acg	gag	gag	atc	ctg	agt	gcc	aat	gcc	acg				432
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr				
	130					135						140							
tac	cag	ctg	ccc	ccc	tgc	atg	ccc	cca	ctg	gat	ctg	aag	tat	gag	gtg				480
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val				
145					150					155					160				
gca	ttc	tgg	aag	gag	ggg	gcc	gga	aac	aag	acc	cta	ttt	cca	gtc	act				528
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr				
				165				170						175					
ccc	cat	ggc	cag	cca	gtc	cag	atc	act	ctc	cag	cca	gct	gcc	agc	gaa				576
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu				
			180					185					190						
cac	cac	tgc	ctc	agt	gcc	aga	acc	atc	tac	acg	ttc	agt	gtc	ccg	aaa				624
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys				
		195					200					205							
tac	agc	aag	ttc	tct	aag	ccc	acc	tgc	ttc	ttg	ctg	gag	gtc	cca	gaa				672
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu				
	210					215					220								
gcc	aac	tgg	gct	ttc	ctg	gtg	ctg	cca	tcg	ctt	ctg	ata	ctg	ctg	tta				720

Ala 225	Asn	Trp	Ala	Phe 230	Leu	Val	Leu	Pro	Ser	Leu 235	Leu	Ile	Leu	Leu	Leu 240	
gta Val	att Ile	gcc Ala	gca Ala	ggg Gly 245	ggt Gly	gtg Val	atc Ile	tgg Trp	aag Lys 250	acc Thr	ctc Leu	atg Met	ggg Gly	aac Asn 255	ccc Pro	768
tgg Trp	ttt Phe	cag Gln 260	cgg Arg	gca Ala	aag Lys	atg Met	cca Pro	cgg Arg 265	gcc Ala	ctg Leu	gac Asp	ttt Phe	tct Ser 270	gga Gly	cac His	816
aca Thr	cac His 275	cct Pro	gtg Val	gca Ala	acc Thr	ttt Phe	cag Gln 280	ccc Pro	agc Ser	aga Arg	cca Pro	gag Glu 285	tcc Ser	gtg Val	aat Asn	864
gac Asp 290	ttg Leu	ttc Phe	ctc Leu	tgt Cys	ccc Pro	caa Gln 295	aag Lys	gaa Glu	ctg Leu	acc Thr	aga Arg 300	ggg Gly	gtc Val	agg Arg	ccg Pro	912
acg Thr 305	cct Pro	cga Arg	gtc Val	agg Arg 310	gcc Ala	cca Pro	gcc Ala	acc Thr	caa Gln 315	cag Gln	aca Thr	aga Arg	tgg Trp	aag Lys	aag Lys 320	960
gac Asp	ctt Leu	gca Ala	gag Glu 325	gac Asp	gaa Glu	gag Glu	gag Glu	gag Glu	gat Asp 330	gag Glu	gag Glu	gac Asp	aca Thr	gaa Glu 335	gat Asp	1008
ggc Gly	gtc Val	agc Ser 340	ttc Phe	cag Gln	ccc Pro	tac Tyr	att Ile	gaa Glu 345	cca Pro	cct Pro	tct Ser	ttc Phe	ctg Leu 350	ggg Gly	caa Gln	1056
gag Glu	cac His 355	cag Gln	gct Ala	cca Pro	ggg Gly	cac His	tcg Ser 360	gag Glu	gct Ala	ggt Gly	ggg Gly	gtg Val 365	gac Asp	tca Ser	ggg Gly	1104
agg Arg 370	ccc Pro	agg Arg	gct Ala	cct Pro	ctg Leu	gtc Val 375	cca Pro	agc Ser	gaa Glu	ggc Gly	tcc Ser 380	tct Ser	gct Ala	tgg Trp	gat Asp	1152
tct Ser 385	tca Ser	gac Asp	aga Arg	agc Ser	tgg Trp 390	gcc Ala	agc Ser	act Thr	gtg Val	gac Asp 395	tcc Ser	tcc Ser	tgg Trp	gac Asp	agg Arg 400	1200

gct ggg tcc tct ggc tat ttg gct gag aag ggg cca ggc caa ggg ccg 1248
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415

ggt ggg gat ggg cac caa gaa tct ctc cca cca cct gaa ttc tcc aag 1296
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430

gac tcg ggt ttc ctg gaa gag ctc cca gaa gat aac ctc tcc tcc tgg 1344
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445

gcc acc tgg ggc acc tta cca ccg gag ccg aat ctg gtc cct ggg gga 1392
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460

ccc cca gtt tct ctt cag aca ctg acc ttc tgc tgg gaa agc agc cct 1440
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480

gag gag gaa gag gag gcg agg gaa tca gaa att gag gac agc gat gcg 1488
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
 485 490 495

ggc agc tgg ggg gct gag agc acc cag agg acc gag gac agg ggc cgg 1536
 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
 500 505 510

aca ttg ggg cat tac atg gcc agg tga 1563
 Thr Leu Gly His Tyr Met Ala Arg *
 515 520

<210> 19

<211> 520

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
 1 5 10 15
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30

Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly
35						40						45			
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr
50						55						60			
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
65				70			75						80		
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
			85						90			95			
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
			100						105			110			
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
115						120						125			
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
130						135						140			
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val
145				150						155			160		
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr
			165						170			175			
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu
			180						185			190			
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys
195						200						205			
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu
210						215						220			
Ala	Asn	Trp	Ala	Phe	Leu	Val	Leu	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu
225				230						235			240		
Val	Ile	Ala	Ala	Gly	Gly	Val	Ile	Trp	Lys	Thr	Leu	Met	Gly	Asn	Pro
			245						250			255			
Trp	Phe	Gln	Arg	Ala	Lys	Met	Pro	Arg	Ala	Leu	Asp	Phe	Ser	Gly	His
			260						265			270			
Thr	His	Pro	Val	Ala	Thr	Phe	Gln	Pro	Ser	Arg	Pro	Glu	Ser	Val	Asn
275						280						285			
Asp	Leu	Phe	Leu	Cys	Pro	Gln	Lys	Glu	Leu	Thr	Arg	Gly	Val	Arg	Pro
290						295						300			
Thr	Pro	Arg	Val	Arg	Ala	Pro	Ala	Thr	Gln	Gln	Thr	Arg	Trp	Lys	Lys
305				310						315			320		
Asp	Leu	Ala	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Asp	Thr	Glu	Asp
			325						330			335			
Gly	Val	Ser	Phe	Gln	Pro	Tyr	Ile	Glu	Pro	Pro	Ser	Phe	Leu	Gly	Gln
			340						345			350			
Glu	His	Gln	Ala	Pro	Gly	His	Ser	Glu	Ala	Gly	Gly	Val	Asp	Ser	Gly
355						360						365			

Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
 370 375 380
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
 385 390 395 400
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
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 Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg Gly Arg
 500 505 510
 Thr Leu Gly His Tyr Met Ala Arg
 515 520

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 <211> 674
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(633)

<400> 20

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gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96
 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30

ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45

aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc	192
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr	
50 55 60	
cgf aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg	240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu	
65 70 75 80	
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc	288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe	
85 90 95	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg	336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	
100 105 110	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct	384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro	
115 120 125	
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg	432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr	
130 135 140	
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg	480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val	
145 150 155 160	
gca ttc tgg aag gag ggg gcc gga aac aag gtg gga agc tcc ttt cct	528
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro	
165 170 175	
gcc ccc agg cta ggc ccg ctc ctc cac ccc ttc tta ctc agg ttc ttc	576
Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe	
180 185 190	
tca ccc tcc cag cct gct cct gca ccc ctc ctc cag gaa gtc ttc cct	624
Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro	
195 200 205	
gta cac tcc tgacttctgg cagtcagccc taataaaatc tgatcaaatg	673
Val His Ser	
210	

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674

<210> 21
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 21

Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln
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 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 20 25 30
 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro
 165 170 175
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe
 180 185 190
 Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro
 195 200 205
 Val His Ser
 210

<210> 22
 <211> 1422
 <212> DNA
 <213> Artificial Sequence

099589.1.201

<220>

<223> Zcytor17-Fc4 fusion protein

<221> CDS

<222> (1)...(1422)

<400> 22

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Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly	
1				5					10					15		

gcc	gtc	ttc	gtt	tcg	ctc	agc	cag	gaa	atc	cat	gcc	gag	ttg	aga	cgc	96
Ala	Val	Phe	Val	Ser	Leu	Ser	Gln	Glu	Ile	His	Ala	Glu	Leu	Arg	Arg	
			20					25					30			

ttc	cgt	aga	tcc	agg	ccc	cgt	ctg	gcc	cct	ccc	cag	aat	gtg	acg	ctg	144
Phe	Arg	Arg	Ser	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu	
			35				40					45				

ctc	tcc	cag	aac	ttc	agc	gtg	tac	ctg	aca	tgg	ctc	cca	ggg	ctt	ggc	192
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly	
	50					55				60						

aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	240
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
65					70				75					80		

cgt	aga	cgg	tgg	cgc	gaa	gtg	gaa	gag	tgt	gcg	gga	acc	aag	gag	ctg	288
Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu	
				85					90					95		

cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc	336
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe	
			100					105					110			

aag	gga	cgc	gtg	cgg	acg	gtt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg	384
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val	
		115					120					125				

gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct	432
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro	
	130					135				140						

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gtc	ctg	gtg	ctc	acc	cag	acg	gag	gag	atc	ctg	agt	gcc	aat	gcc	acg	480
Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	
145					150					155					160	
tac	cag	ctg	ccc	ccc	tgc	atg	ccc	cca	ctg	gat	ctg	aag	tat	gag	gtg	528
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val	
				165					170					175		
gca	ttc	tgg	aag	gag	ggg	gcc	gga	aac	aag	acc	cta	ttt	cca	gtc	act	576
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr	
			180					185					190			
ccc	cat	ggc	cag	cca	gtc	cag	atc	act	ctc	cag	cca	gct	gcc	agc	gaa	624
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu	
		195					200					205				
cac	cac	tgc	ctc	agt	gcc	aga	acc	atc	tac	acg	ttc	agt	gtc	ccg	aaa	672
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys	
	210					215					220					
tac	agc	aag	ttc	tct	aag	ccc	acc	tgc	ttc	ttg	ctg	gag	gtc	cca	gaa	720
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu	
225					230					235					240	
gcc	aac	tgg	aga	tct	tca	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	768
Ala	Asn	Trp	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	
				245					250					255		
gca	cct	gaa	gcc	gag	ggg	gca	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	816
Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	
			260					265					270			
ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	864
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
		275					280					285				
gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	912
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	
	290					295					300					
gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	960
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	
305					310					315					320	

cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac	1008
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His	
325 330 335	
cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa	1056
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys	
340 345 350	
gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc aaa ggg cag	1104
Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln	
355 360 365	
ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg	1152
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu	
370 375 380	
acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc	1200
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro	
385 390 395 400	
agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac	1248
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn	
405 410 415	
tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc	1296
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu	
420 425 430	
tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc	1344
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val	
435 440 445	
ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag	1392
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln	
450 455 460	
aag agc ctc tcc ctg tct ccg ggt aaa taa	1422
Lys Ser Leu Ser Leu Ser Pro Gly Lys *	
465 470	

<211> 473

<212> PRT

<213> Artificial Sequence

<400> 23

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Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
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			100				105						110		
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
		115					120						125		
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
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145					150					155				160	
Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val
				165					170					175	
Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr
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Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu
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	210					215					220				
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu
225					230					235				240	
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				245					250					255	
Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
		260					265						270		
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
		275					280						285		
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
	290					295							300		

FORM 1-12-60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 305 310 315 320
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 325 330 335
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 340 345 350
 Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 355 360 365
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 370 375 380
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 385 390 395 400
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 405 410 415
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 420 425 430
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
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28

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<212> DNA

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N0:19

<221> misc_feature

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<223> n = A,T,C or G

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ytnacntggy tncnggny nggnaayccn cargaygt na cntayttygt ngcntaycar	180
wsnwsnccna cmgmngmng ntggmngar gtngargart gygcnggnac naargarytn	240
ytntgywsna tgatgtggyt naaraarcar gayytnaya ayaarttyaa rggnmgngtn	300

mgnacngtnw	sncnwsnws	naarwsnccn	tgggtngarw	sngartayyt	ngaytayytn	360
ttygargtn	arccngcncc	nccngtnytn	gtnytnacnc	aracngarga	rathytnwsn	420
gcnaaygcna	cntaycaryt	nccncntgy	atgccnccny	tngayytnaa	rtaygargtn	480
gcnttytgga	argarggngc	nggnaayaar	acnytnnttyc	cngtnacncc	ncayggncar	540
ccngtncara	thacnytnca	rcngcngcn	wsngarcayc	aytggytnws	ngcnmgnacn	600
athtayacnt	tywsngtncc	naartaywsn	aarttywsna	arccnacntg	ytttytnytn	660
gargtnccng	argcnaaytg	ggcnttyytn	gtnytnccnw	snytnytnat	hytnytnytn	720
gtnathgcng	cngggngngt	nathtggaar	acnytnatgg	gnaayccntg	gttycarmgn	780
gcnaaratgc	cnmgngcny	ngayttywsn	ggncayacnc	ayccngtngc	nacnttycar	840
ccnwsnmgnc	cngarwsngt	naaygayytn	ttyytnntgy	cncaraarga	rytnacnmgn	900
ggngtnmgnc	cnacnccnmg	ngtnmgngcn	ccngcnacnc	arcaracnmg	ntggaaraar	960
gayytnccng	argaygarga	rgargargay	gargargaya	cngargaygg	ngtnwsntty	1020
carccntaya	thgarccncc	nwsnttyytn	ggncargarc	aycargcncc	nggncaywsn	1080
gargcnggng	gngtngayws	nggnmgncn	mgngcnccny	tngtnccnws	ngarggnwsn	1140
wsngcntggg	aywsnwsnga	ymgnwsntgg	gcnwsnacng	tngaywsnws	ntgggaymgn	1200
gcnggnwsnw	snggntayyt	ngcngaraar	ggncnccngc	arggncnccng	nggngayggn	1260
caycargarw	snytnccncc	nccngartty	wsnaargayw	snggnttyyt	ngargarytn	1320
ccngargaya	ayytnwsnws	ntgggcnacn	tggggnacny	tccnccnga	rccnaayytn	1380
gtncnccngg	gncnccngt	nwsnytnear	acnytnacnt	tytgytgga	rwsnwsnccn	1440
gargargarg	argargcnmg	ngarwsngar	athgargayw	sngaygcngg	nwsntggggn	1500
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<221> misc_feature

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ytnacntggy	tncnccngny	nggnaayccn	cargaygtna	cntayttygt	ngcntaycar	180
wsnwsnccna	cnmgmngmng	ntggmngar	gtngargart	gygcnggnac	naargarytn	240
ytnygywsna	tgatgtgyyt	naaraarcar	gayytnntaya	ayaarttyaa	rggnmgngtn	300
mgnacngtnw	sncnwsnws	naarwsnccn	tgggtngarw	sngartayyt	ngaytayytn	360
ttygargtn	arccngcncc	nccngtnytn	gtnytnacnc	aracngarga	rathytnwsn	420
gcnaaygcna	cntaycaryt	nccncntgy	atgccnccny	tngayytnaa	rtaygargtn	480

gcnttytgga argarggngc nggnaayaar gtnggnwsnw snttyccngc nccnmgnytn 540
 ggncnytny tncayccntt yytnytnmgn ttyttywsnc cnwsncarcc ngcnccngcn 600
 ccnytnytn argargtntt yccngtncay wsn 633

<210> 30

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Primer ZC39204

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 ccag 64

<210> 31

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Primer ZC39205

<400> 31

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 ccag 64

<210> 32

<211> 1922

<212> DNA

<213> Artificial Sequence

<220>

<223> MBP-human zcytoR19 fusion protein polynucleotide
 sequence

<221> CDS

<222> (123)...(1922)

<400> 32

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 caggaaacag ccagtccgtt taggtgtttt cacgagcact tcaccaacaa ggaccataga 120

tt atg aaa act gaa gaa ggt aaa ctg gta atc tgg att aac ggc gat	167
Met Lys Thr Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp	
1 5 10 15	
aaa ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat	215
Lys Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp	
20 25 30	
acc gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa	263
Thr Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys	
35 40 45	
ttc cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg	311
Phe Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp	
50 55 60	
gca cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa	359
Ala His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu	
65 70 75	
atc acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg	407
Ile Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp	
80 85 90 95	
gat gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt	455
Asp Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val	
100 105 110	
gaa gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca	503
Glu Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro	
115 120 125	
aaa acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa	551
Lys Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys	
130 135 140	
ggt aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg	599
Gly Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp	
145 150 155	
ccg ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc	647
Pro Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly	
160 165 170 175	

aag tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg	695
Lys Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala	
180 185 190	
ggt ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca	743
Gly Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala	
195 200 205	
gac acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca	791
Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr	
210 215 220	
gcg atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc	839
Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser	
225 230 235	
aaa gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca	887
Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro	
240 245 250 255	
tcc aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt	935
Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser	
260 265 270	
ccg aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act	983
Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr	
275 280 285	
gat gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta	1031
Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val	
290 295 300	
gcg ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc	1079
Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala	
305 310 315	
gcc acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg	1127
Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro	
320 325 330 335	
cag atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc	1175

Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala	
340 345 350	
gcc agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act	1223
Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr	
355 360 365	
aat tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg	1271
Asn Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu	
370 375 380	
gtt ccg cgt gga tcc agg ccc cgt ctg gcc cct ccc cag aat gtg acg	1319
Val Pro Arg Gly Ser Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr	
385 390 395	
ctg ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt	1367
Leu Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu	
400 405 410 415	
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Gly Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro	
420 425 430	
acc cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag	1463
Thr Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu	
435 440 445	
ctg cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag	1511
Leu Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys	
450 455 460	
ttc aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg	1559
Phe Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp	
465 470 475	
gtg gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca	1607
Val Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro	
480 485 490 495	
cct gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc	1655
Pro Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala	
500 505 510	

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acg tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag 1703
 Thr Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu
 515 520 525

gtg gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc 1751
 Val Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val
 530 535 540

act ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc 1799
 Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser
 545 550 555

gaa cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg 1847
 Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro
 560 565 570 575

aaa tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca 1895
 Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro
 580 585 590

gaa gcc aac tgg tgt ttt ggc gga tga 1922
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<212> PRT

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<220>

<223> MBP-human zcytoR19 fusion protein polypeptide
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 20 25 30
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60

0995898-112801

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val
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0995898-112801

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Asn Phe Ser Val
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 gccccagcca cccaacagac aaga 24

<210> 36
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<220>
 <223> Oligonucleotide primer ZC40286

<400> 36
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<210> 37
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<400> 37
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<210> 38
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<210> 39
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<210> 40
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<400> 40
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<400> 41
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<400> 42

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cccttcctgc tcctttgact gcgt

24

<210> 43
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 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC39408

<400> 43
 gccccagctgc atcttcctag aggc

24

<210> 44
 <211> 25
 <212> DNA
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 <223> Oligonucleotide primer ZC39409

<400> 44
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25

<210> 45
 <211> 121
 <212> DNA
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<220>
 <223> forward zcytor19 knockout oligonucleotide

<400> 45
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 cggccggccc ctaggatccg aattctagaa gctttgtgtc tcaaaatctc tgatgttaca 120
 t 121

<210> 46
 <211> 125
 <212> DNA
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<220>

009589-1201

<223> reverse zcytor19 knockout oligonucleotide

<400> 46

ggctggtccc ctgcaagagt agcaagcgct tcttcagcat ccggacttac ggcctcgctg	60
gccggcgcg ctaggaattc tctagaggat ccaagctttt agaaaaactc atcgagcatc	120
aatg	125

<210> 47

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38481

<400> 47

cctccttcca gaatgccacc tc	22
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<210> 48

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38626

<400> 48

ctgctatgtt ctatgatgtg cctga	25
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<210> 49

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38706

<400> 49

ggaagataat gaaaggaaac cc	22
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<210> 50

<211> 21

<212> DNA

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<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38711

<400> 50

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21

0995898-11301
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